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Abstracts
Germ Cells and Gametogenesis

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Identification of dominant suppressors of the *fog-1*(*q253*ts) allele

Kristin R. Douglas, Meaghan E. Bychowski, Kevin S. Nelson
Augustana College, Rock Island, IL, USA

Germ cell fate in *C. elegans* is determined by a complex genetic pathway ending in *fog-1* and *fog-3*. FOG-1 is a cytoplasmic polyadenylation element binding (CPEB) protein which is required for germ cell proliferation and spermatogenesis. CPEB proteins bind to CPEs of target mRNAs to regulate their translation. In *Xenopus*, CPEB protein interacts with Maskin or cleavage and polyadenylation specificity factor (CPSF) to regulate translation of its targets. Such partners of FOG-1 remain largely unknown. To elucidate how FOG-1 regulates cell fate and cell proliferation in *C. elegans* germ cells, we have initiated a genetic suppressor screen looking for dominant suppressors of the *fog-1*(*q253*ts) allele. We expect to identify proteins that either regulate or interact with FOG-1. We have mutagenized approximately 85,000 haploid genomes and identified two dominant suppressors of *fog-1*(*q253*ts). We are currently characterizing the suppressor mutations.

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BMP signaling within the urogenital ridges supports PGC survival and migration

Kathleen Molyneaux, Brian Dudley, Jennifer Nalepka
Case Western Reserve University, Cleveland, OH, USA

Primordial germ cells (PGCs) are the embryonic precursors of the gametes. Members of the bone morphogenetic protein (BMP) family induce formation of PGCs within the proximal epiblast of the E7.5 mouse embryo. After formation, PGCs proliferate and migrate to the urogenital ridges, the structures that will develop into the gonads. Using an organ culture system and live cell confocal microscopy, we identified a novel role for BMPs in controlling PGC numbers and motility as they colonize the UGRs. BMPs do not act as guidance factors for PGCs; instead BMP signaling within the urogenital ridges acts to control localized expression of the germ cell survival factor *Kit ligand* (*Kitl*). Tissue specific targeting of *Bmpr1a* is being used to confirm the role of BMP signaling in PGC migration in vivo. BMPs control expression of *Kitl* within the granulosa cells of the adult ovary; hence, this signaling process is used at multiple stages of development to regulate interactions between germ cells and soma.

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Targeting GLH function in *C. elegans* P granules

Erica L. Racen, Karen L. Bennett
University of Missouri-Columbia, MO, USA

P granules are ribonucleoprotein aggregates that segregate to the *C. elegans* germline lineage throughout development. Our laboratory is interested in better understanding the role of the four P granule associated Germline RNA Helicase proteins (GLHs). The GLH proteins are the homologues of the *Drosophila* protein Vasa. The Lasko laboratory has shown that Vasa is involved in the translational control of mRNAs associated with polar granules when in complex with other protein binding partners. To better elucidate GLH protein function, we have begun looking at protein binding partners of GLH-1 through immunoprecipitation (IP) experiments using whole worm extracts. To date, one candidate protein has been identified; that GLH binding partner is PGL-1, which is also a P granule-associated protein. While PGL-1 and GLH-1 are known to interact genetically, the physical interaction of PGL-1 with GLH-1 has not been previously reported. In our studies, GLH-1 appears to bind PGL-1 and this interaction is dependent on the presence of RNA. We intend to determine whether specific RNAs are bound. We are also attempting to produce a GLH-1::GFP transgenic worm. To make a germline expressing transgenic strain, we are using micro-particle bombardment of worms that are homozygous for both the *unc-119(ed3)* and *glh-1(ok439)* mutations (the construct, containing wild-type *unc-119(ed3)* and *glh-1(ok439)* selects for the rescue of the *unc-119* phenotype along with the rescue of sterility of the *glh-1(ok439)* strain).